

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2001, 19:13:06 ; Search time 2802.37 Seconds

(Without alignments)
23323.767 Million cell updates/sec

File: US-08-153-397A-1

Sequence: 1 CGGCGCTGAGACTGGGCTCA.....AAAAAAAAAACCGAATTC 3962

Scoring table: IDENTITY_NUC 1
Gapop 10.0, Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

GenEmbl: 1: gb_da: 2: gb_hlg: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_da: 16: em_fun: 17: em_hum: 18: em_in: 19: em_om: 20: em_ov: 21: em_ov: 22: em_pat: 23: em_ph: 24: em_pl: 25: em_ro: 26: em_sts: 27: em_sy: 28: em_un: 29: em_vl: 30: em_hlgo_hum: 31: em_hlgo_inv: 32: em_hlgo_rod: 33: em_hlgo_hum: 34: em_hlg_inv: 35: em_hlg_rod: 36: em_hlg_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3962	100.0	3962	6	I68738
2	3625.6	91.5	3754	6	A42378
3	3619.2	91.3	3738	9	HUMTRK
4	3613.4	91.2	3849	9	BC008716
5	3544.4	89.3	3803	9	HUMCAR
6	3451	87.1	3637	6	AR094160
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8	3451	87.1	3637	6	AR105288
9	3451	87.1	3637	6	AR10845
10	3383.2	85.4	3554	9	HSTRKE
11	3366	83.0	3841	9	HSRETYK1
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13	2405.6	60.7	3659	10	AF026259
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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 1 from patent US 5677144.
ACCESSION I68738
VERSION I68738.1 GI:2830860
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3962)
AUTHORS Dillrich,A. and Alves,F.HildgardElisabeth.
TITLE Recombinant DNA encoding CCK 2, a receptor tyrosine kinase
JOURNAL Patent: US 5677144-A 1 14-OCT-1997;
FEATURES
source 1. 3962
BASE COUNT 735 a 1234 c 1182 g 811 t
ORIGIN

Query Match 100.0%; Score 3962; DB 6; Length 3962;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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BASE COUNT 712 a 1146 c 1121 g 775 t
ORIGIN

Query Match 91.5%; Score 3625.6; DB 6; Length 3754;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 3733; Conservative 0; Mismatches 14; Indels 29; Gaps 7;

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DB 62 TCAGTGAAGATGGGTGGACTTGAAGAAATCCCAAGATGCTGCCCCACCCCTTA 121
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DB 482 TGCACCGAGGATGAGAGTGTCTCCCAAGAGAGTGTGCGCGGCTGGGCTGGAAG 541
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DB 542 ACCGCTGGGATGAGAGTGTCTGAGCAATGAGAGACCTGAGGAGTGTGCTGAAG 601

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 AUTHORS Strausberg, R.
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 JOURNAL Submitted (25-MAY-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 CONTACT: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
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 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
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ACCESSION L20817

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VERSION L20817.1 GI:306474
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ORGANISM Homo sapiens
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AUTHORS Perez,J.L., Shen,X., Finkernagel,S., Sclorraj,L., Jenkins,N.A.,
Gilbert,D.J., Copeland,N.G. and Wong,T.W.
TITLE Identification and chromosomal mapping of a receptor tyrosine
kinase with a putative phospholipid binding sequence in its
ectodomain
Oncogene 9, 211-219 (1994)
MEDLINE 94134417
REFERENCE 2 (bases 1 to 3803)
AUTHORS Johnson,J.D.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-1993) J.D. Johnson
REFERENCE 3 (sites)
AUTHORS Johnson,J.D., Edman,J.C. and Rutter,W.J.
TITLE A receptor tyrosine kinase found in breast carcinoma cells has an
extracellular discoidin I-like domain
Proc. Natl. Acad. Sci. U.S.A. 90, 5677-5681 (1993)
JOURNAL 53296201
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Best Local Similarity 96.9%; Pred. No. 0;

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Matches 3765: Conservative 0; Mismatches 21; Indels 98; Gaps 11;

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QY 76 GCGTCCCGACACCGAGCCCGCGGCGCTCCCGCTCCCGGCTCCG-----GCTCCT 129
Db 1 GCGTCCCGACACCGAGCCCGCGGCGCTCCCGCTCCCGGCTCCCGGCTCCG 59
QY 130 GCGTCCCGTCCCGGCTCCCGGCTCCCGGCTCCCGGCTCCCGGCTCCG 189
Db 60 GCGTCCCGTCCCGGCTCCCGGCTCCCGGCTCCCGGCTCCCGGCTCCG 117
QY 190 GACGCTCGGCTCCCGGCTCCCGGCTCCCGGCTCCCGGCTCCG 249
Db 118 GACGCTCGGCTCCCGGCTCCCGGCTCCCGGCTCCCGGCTCCG 148
QY 250 GATGGGCTGGAGTGAAGGATGGAGAGTGGTCCCGGCTCCCGGCTCCG 309
Db 149 -----AGAGATGCTGCCCGCCCGCTTGGCGCGAG 181
QY 310 GATCAGAGATGAGGAGCAGAGCGCTGTCATCTTACTGCTGCTGCTGCTGAG 369
Db 182 GATCAGAGATGAGGAGCAGAGCGCTGTCATCTTACTGCTGCTGCTGCTGAG 241
QY 370 GTGAGATGCTGACATGAGGAGGACATTTGATCCCGCAAGTCCGCTATGCCGCA 429
Db 242 GTGAGATGCTGACATGAGGAGGACATTTGATCCCGCAAGTCCGCTATGCCGCA 301
QY 430 TGCAGAGCCGAGACCATCCCAACAGTGCATCTGCTCCAGCTCCGCTGAGATCCA 489
Db 302 TGCAGAGCCGAGACCATCCCAACAGTGCATCTGCTCCAGCTCCGCTGAGATCCA 361
QY 490 CTGCGCGCCGCGACAGGAGTGGAGAGCAGTGAAGGAGGAGGAGGAGGAGGAG 549
Db 362 CTGCGCGCCGCGACAGGAGTGGAGAGCAGTGAAGGAGGAGGAGGAGGAGGAG 421
QY 550 GGTGCGGTGTTCCCAAGAGAGAGGAGTACTTGCAGGTGATCTACACAGCATCCAG 609
Db 422 GGTGCGGTGTTCCCAAGAGAGAGGAGTACTTGCAGGTGATCTACACAGCATCCAG 481
QY 610 TGGCTCTGCTGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 669
Db 482 TGGCTCTGCTGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 541
QY 670 GTCACCGGCTGCGTACTCCCGGAGTGGTGGCGCTGATGGGCTGGAAGACCGCTGG 729
Db 542 GTCACCGGCTGCGTACTCCCGGAGTGGTGGCGCTGATGGGCTGGAAGACCGCTGG 601
QY 730 GTCAGAGAGTGTATCTAGGAGCAATGAGAGCCCTGAGGAGGAGTGTCTAAGACCTTGGGC 789
Db 602 GTCAGAGAGTGTATCTAGGAGCAATGAGAGCCCTGAGGAGGAGTGTCTAAGACCTTGGGC 661
QY 790 CCCCCATGCTGCCCCGAGTGGTTCGCTTCAACCCCGGCTGACCGGCTATGAGCTCT 849
Db 662 CCCCCATGCTGCCCCGAGTGGTTCGCTTCAACCCCGGCTGACCGGCTATGAGCTCT 721
QY 850 GTCGTGGGGAGAGGCTATAGGCTGCTGCTGAGAGGAGTGAATCTCTTACACCGCCC 909
Db 722 GTCGTGGGGAGAGGCTATAGGCTGCTGCTGAGAGGAGTGAATCTCTTACACCGCCC 781
QY 910 CTGTGGGGAGAGCAATGTATTTATCTGAGGCGCTGTACTCAAGAGATCCACCATATAG 969
Db 782 CTGTGGGGAGAGCAATGTATTTATCTGAGGCGCTGTACTCAAGAGATCCACCATATAG 841
QY 970 GACATACCGTGGGCGAGTGCATATGAGGCTGAGGCGAGCTGGCAGATGCTGTGGTGG 1029
Db 842 GACATACCGTGGGCGAGTGCATATGAGGCTGAGGCGAGCTGGCAGATGCTGTGGTGG 901
QY 1030 GAGTGAATGCTTTAGGAGAGTCAAGAGCTGGGGCTGTGGCGCAAGCTATGACTATGTGG 1089
Db 902 GAGTGAATGCTTTAGGAGAGTCAAGAGCTGGGGCTGTGGCGCAAGCTATGACTATGTGG 961
QY 1090 GATGAGAGCAACAGACTTCTCCAGTGGCTATGTGAGATGAGATTGATTTGACCGGC 1149
Db 962 GATGAGAGCAACAGACTTCTCCAGTGGCTATGTGAGATGAGATTGATTTGACCGGC 1021
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QY 1150 TGAAGGCTTCCAGGCTATGACAGTCCACTGTAAACAATGCAACAGCTGGAGCCCTTC 1209
Db 1022 TGAAGGCTTCCAGGCTATGACAGTCCACTGTAAACAATGCAACAGCTGGAGCCCTTC 1081
QY 1210 TGGCTGGCGGGGAGGAGTGTGCTTCCGCGCTGAGGCTGCTGCTGAGGAGGAGGAG 1269
Db 1082 TGGCTGGCGGGGAGGAGTGTGCTTCCGCGCTGAGGCTGCTGCTGAGGAGGAGGAG 1141
QY 1270 CCATGGCCCAACCTAGAGGAGGAGCACTGGGGAGACCCAGAGCGGGGCTGCTGAGTGC 1329
Db 1142 CCATGGCCCAACCTAGAGGAGGAGCACTGGGGAGACCCAGAGCGGGGCTGCTGAGTGC 1201
QY 1330 CCGTGGCGGGGCTGAGTGTGCTTCTGAGGCTTCTGAGGCTTCTTGGGGGCGCTGGT 1389
Db 1202 CCGTGGCGGGGCTGAGTGTGCTTCTGAGGCTTCTGAGGCTTCTTGGGGGCGCTGGT 1261
QY 1390 TACTCTTACGCAATCTCTTCATCTGTATGTGTGAACAATTCCTCCGAGACTGG 1449
Db 1262 TACTCTTACGCAATCTCTTCATCTGTATGTGTGAACAATTCCTCCGAGACTGG 1321
QY 1450 GAGGACCTTCCGCGAGCGCCGCTGGTGGCGGCTGAGGCTCCAGCAACTTCAGCA 1509
Db 1322 GAGGACCTTCCGCGAGCGCCGCTGGTGGCGGCTGAGGCTCCAGCAACTTCAGCA 1381
QY 1510 GCTTGGAGCTGAGGCCAGAGAGCCAGAGCCGCTGAGCAGAGGCGAGGAGGAGGAG 1569
Db 1382 GCTTGGAGCTGAGGCCAGAGAGCCAGAGCCGCTGAGCAGAGGCGAGGAGGAGGAG 1441
QY 1570 CCATCTTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1629
Db 1442 CCATCTTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1501
QY 1630 TGCCTTGGCGGGTGCAGCTGGGCGAGGCTCTGAGCAAGGCTGAGAGGAGGCTTGGAG 1689
Db 1502 TGCCTTGGCGGGTGCAGCTGGGCGAGGCTCTGAGCAAGGCTGAGAGGAGGCTTGGAG 1561
QY 1690 AGGAGCTGACGGTTCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1749
Db 1562 AGGAGCTGACGGTTCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1621
QY 1750 GTCTTAGAGAGCAACCCCGCTAGCAAGAGCCCGGCTGCTGAGGAGTCCGCGCCCACTCG 1809
Db 1622 GTCTTAGAGAGCAACCCCGCTAGCAAGAGCCCGGCTGCTGAGGAGTCCGCGCCCACTCG 1661
QY 1810 CTCCCTGTGTCCCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1869
Db 1682 CTCCCTGTGTCCCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1741
QY 1870 TGGCCACTTACGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1929
Db 1742 TGGCCACTTACGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1801
QY 1930 CCACCAACACCCAGGCTTACAGTGGGAGTATATGAGAGCTGAGAGGCGCAGAGCCCGCGC 1989
Db 1802 CCACCAACACCCAGGCTTACAGTGGGAGTATATGAGAGCTGAGAGGCGCAGAGCCCGCGC 1861
QY 1990 TTTCTGCCCCCAGCTTCCCGAGAACAGGCTCCCATATATGCCAGGCTGACATTTTACC 2049
Db 1862 TTTCTGCCCCCAGCTTCCCGAGAACAGGCTCCCATATATGCCAGGCTGACATTTTACC 1921
QY 2050 TGCAGGGCGTCAACGCGGGGAGCAACACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2109
Db 1922 TGCAGGGCGTCAACGCGGGGAGCAACACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1981
QY 2110 GGGATGGGCCCCCGAGATGATTTCCCTGATCTGCACTCCGCTTCAAGAGAAAGCTTG 2169
Db 1982 GGGATGGGCCCCCGAGATGATTTCCCTGATCTGCACTCCGCTTCAAGAGAAAGCTTG 2041
QY 2170 GCGAGGGCGGCTTGGGAGGAGTGCATCTGTGTGAGTGCAGAGCCCTCAAGATCTGGTCA 2229
Db 2042 GCGAGGGCGGCTTGGGAGGAGTGCATCTGTGTGAGTGCAGAGCCCTCAAGATCTGGTCA 2101
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QY	316	GAGCTATGGGACCCAGAGGCCCTGTCACTCTTACTGCTGCTGCTCTGGTGCGCAATGGAG	375
Db	77	GAGCTATGGGACCCAGAGGCCCTGTCACTCTTACTGCTGCTGCTCTGGTGCGCAATGGAG	136
QY	376	ATGCTGACATGAAGGAGACATTTTGAATCTGTGCGCAAGTGGCCGCTATGCCCTGGGCAATGCAG	435
Db	137	ATGCTGACATGAAGGAGACATTTTGAATCTGTGCGCAAGTGGCCGCTATGCCCTGGGCAATGCAG	196
QY	436	ACCGGACCATCCAGACAGTACATCTCTGCTCCAGCTCCGTGCGACAGATTCACATGCGCG	495
Db	197	ACCGGACCATCCAGACAGTACATCTCTGCTCCAGCTCCGTGCGACAGATTCACATGCGCG	256
QY	496	CCGCGCAAGAGGTTGGAGAGCAGTGACGCGGAGTGGGGCTGTGTCGCCCGCAGAGGTGCG	555
Db	257	CCGCGCAAGAGGTTGGAGAGCAGTGAGCGGAGTGGGGCTGTGTCGCCCGCAGAGGTGCG	316
QY	556	TGTTTCCCAAGAGGAGAGAGTACTTGTGCAAGTGTGATCTTCAACGACTCCACTGTGTGCTC	615
Db	317	TGTTTCCCAAGAGGAGAGAGTACTTGTGCAAGTGTGATCTTCAACGACTCCACTGTGTGCTC	376
QY	616	TGGTGGGCGACCCAGAGGAGCGGATCCCGGGGGCTGGGGCAAGAGTTCGCCGGACTCCAC	675
Db	377	TGGTGGGCGACCCAGAGGAGCGGATCCCGGGGGCTGGGGCAAGAGTTCCTCCGGAGCTACC	436
QY	676	GCGTGGCTACTCCCGGGATGTCGCCGCTGGATGGGCTGGAGAACCGCTGGGGGTACAG	735
Db	437	GCGTGGCTACTCCCGGGATGTCGCCGCTGGATGGGCTGGAGAACCGCTGGGGGTACAG	496
QY	736	AGGTGATCTAGGCAATAGAGGACCCCTAGAGGAGTGTGTCTAAGAGACCTTGGGCCCCCA	795
Db	497	AGGTGATCTAGGCAATAGAGGACCCCTAGAGGAGTGTGTCTAAGAGACCTTGGGCCCCCA	556
QY	796	TGGTTGCCACACTGTTGCTCGCTTACACCCCGGGGCTGACCGGGTATGAGTCTGTCTGCG	855
Db	557	TGGTTGCCACACTGTTGCTCGCTTCTACCCCGGGGCTGACCGGGTATGAGTCTGTCTGCG	616
QY	856	GGGTAGAGCTTATGGCTGCTCTGAGGAGTGAAGTCTGTCTTACACCCGCCCTGTGG	915
Db	617	GGGTAGAGCTTATGGCTGCTCTGAGGAGTGAAGTCTGTCTTACACCCGCCCTGTGG	676
QY	916	GGGAGCAATGTATTTATCTGAGGGCCGTATACCTCAACGACTCCACTATACGCACTA	975
Db	677	GGGAGCAATGTATTTATCTGAGGGCCGTATACCTCAACGACTCCACTATACGCACTA	736
QY	976	CCGTGGGCGACACTGCAATATGCGGGTGTGGGCCAGTGGGAGTGGTGGGGCGCG	1035
Db	737	CCGTGGGCGACACTGCAATATGCGGGTGTGGGCCAGTGGGAGTGGTGGGGCGCG	796
QY	1036	ATGACTTTAGGAAGAGTCAAGAGCTGGGGTCTGGCCAGGCTATGACTATGTGGGATGA	1095
Db	797	ATGACTTTAGGAAGAGTCAAGAGCTGGGGTCTGGCCAGGCTATGACTATGTGGGATGA	856
QY	1096	GCAACCAAGCTCTCCAGTGGCTATGTGGAGTGGAGTTGAGTTTACCGGCTGAGGG	1155
Db	857	GCAACCAAGCTCTCCAGTGGCTATGTGGAGTGGAGTTGAGTTTACCGGCTGAGGG	916
QY	1156	CCCTTCAGGCTATGAGGTCCTACTGTAAACAATGACAGCGTGGAGGCCGTGTGCTG	1215
Db	917	CCCTTCAGGCTATGAGGTCCTACTGTAAACAATGACAGCGTGGAGGCCGTGTGCTG	976
QY	1216	GCGGGGTGAATGTGCTTCGGCGTGGCCCTGTCATAGGCTGGGAGGGGAGGCCATGC	1275
Db	977	GCGGGGTGAATGTGCTTCGGCGTGGCCCTGTCATAGGCTGGGAGGGGAGGCCATGC	1036
QY	1276	GCCACAACCTAGGGGGGCAACCTGGGGGAGCCCGAGAGCCGGGCTGTCAAGTGCCTTG	1335
Db	1037	GCCACAACCTAGGGGGGCAACCTGGGGGAGCCCGAGAGCCGGGCTGTCAAGTGCCTTG	1096
QY	1336	GCGGCGGTGTGGCTGCTTCTCTCAGTGGCGGCTTCCTTGGGGGGCCGTGTACTCT	1395
Db	1097	GCGGCGGTGTGGCTGCTTCTCTCAGTGGCGGCTTCCTTGGGGGGCCGTGTACTCT	1156
QY	1396	TCAGGCAAAATCTCTCATCTGTGATGTGGTGAACAATTCCTCCGCGCATGTGGAGCA	1455

Db	1157	TCAGCGAATCTCCTTACTCTATGTGGGAACAATTCTTCGCGCACTGGGGCA	1216
QY	1456	CCTTCCCGCAAGCCCCGTTGGCGCCTGGGCCCACTCCCAACAATTACAGACTTGG	1515
Db	1217	CCATCCCGGACAGCCCTCTGTGGGCGCTGGCCCACTCCCAACAATTACAGACTTGG	1276
QY	1516	AGCTGAGCGCCAGAGAGCCAGACGCCCTGGGCCAAGGCCGAGGGGAGCCGACCGCCATCC	1573
Db	1277	AGCTGAGCGCCAGAGAGCCAGAGCGCCGTGGCCAAAGCCGAGGGGAGCCGACCGCCATCC	1336
QY	1576	TCATGGGCGCCTGGTGGCCATACACTGGCCCTGGCGCAATCATTTGCCATCAGTCT	1633
Db	1337	TCATGGGCGCCTGGTGGCCATCATCTGCTCTGGCGCAATCATTTGCCATCAGTCT	1396
QY	1636	GGCGGCTGACTGTGGCGAGCGCTCCTCAGCAAGGCTGAACGAGAGGTTGGAAAGAGAGC	1699
Db	1397	GGCGGCTGAGTGGGCGAGGCTCCTCAGCAAGGCTGAACGAGAGGTTGGAAAGAGAGC	1456
QY	1696	TCACGTTACACTCTCTGTCCCTGGGAGACATATCTCATCAACACGCGCAGGTCCCTA	1755
Db	1457	TCACGTTACACTCTCTGTCCCTGGGAGACATATCTCATCAACACGCGCAGGTCCCTA	1516
QY	1756	GAGAGCAACCCCGGACAGGAGGCCCGGCGCTGTGGGAATCCGCCCACTCCGCTCCT	1815
Db	1517	GAGAGCAACCCCGGACAGGAGGCCCGGCGCTGTGGGAATCCGCCCACTCCGCTCCT	1576
QY	1816	GTGTCCCAATGGCTCTGCTGTGTCTCTCAATCCAGGCTTACCGCTCTTTGGGCA	1875
Db	1577	GTGTCCCAATGGCTCTGCTGTGTCTCTCAATCCAGGCTTACCGCTCTTTGGGCA	1633
QY	1876	CTTACGCGCCGTCCTCGAGGCGCGGGCCGCCACACACCGCGCTGGGCCAAACCCACA	1935
Db	1637	CTTACGCGCCGTCCTCGAGGCGCGGGCCGCCACACACCGCGCTGGGCCAAACCCACA	1696
QY	1936	ACACCCAGGCGCTAAGTGGGGAGCTATATGAGGCTGAGAAAGCAGGCGCCCGCTTCTGC	1995
Db	1697	ACACCCAGGCGCTAAGTGGGGAGCTATATGAGGCTGAGAAAGCAGGCGCCCGCTTCTGC	1756
QY	1996	CCCCACCTCCCAAGACAGCTCCCGCATATGCGAGGCGTGACATGTTACCCGACAG	2055
Db	1757	CCCCACCTCCCAAGACAGCTCCCGCATATGCGAGGCGTGACATGTTACCCGACAG	1816
QY	2056	GGTCACCGGGGGGACACCTATGCTGTGCTGCTACGTGCCCGCAGGGGAGCAGTGGGATG	2115
Db	1817	GGTCACCGGGGGGACACCTATGCTGTGCTGCTACGTGCCCGCAGGGGAGCAGTGGGATG	1876
QY	2116	GGCCCCCAAGTGGATTCCCTCGATCTCGACTCCGCTTCAAGGAGAACTTGGCGAGG	2175
Db	1877	GGCCCCCAAGTGGATTCCCTCGATCTCGACTCCGCTTCAAGGAGAACTTGGCGAGG	1936
QY	2176	GGCAATTTGGGAGAGTCACTGTGTGTGAGGTGACAGCGCCCTCAAAATCTGGTCAATCTTG	2235
Db	1937	GGCAATTTGGGAGAGTCACTGTGTGTGAGGTGACAGCGCCCTCAAAATCTGGTCAATCTTG	1996
QY	2236	ATTTCCCGCTTAATGTGCTGAAGGAGACCCCTTGGTGTAGCTGTCAAGATCTTACGCG	2295
Db	1997	ATTTCCCGCTTAATGTGCTGAAGGAGACCCCTTGGTGTAGCTGTCAAGATCTTACGCG	2056
QY	2296	CAGATGCCACCAAGATGCCAGCTTCTCTGTCTCAGGAATGATTTCTGAAAGAG	2355
Db	2057	CAGATGCCACCAAGATG-----CAGGAATGATTTCTGAAAGAG	2098
QY	2356	TGAAGATCATGTGAGGCTCAAGAGCCCAACAATCATTTGGGTGCTGGGCGTGTGTGTGC	2415
Db	2099	TGAAGATCATGTGAGGCTCAAGAGCCCAACAATCATTTGGGTGCTGGGCGTGTGTGTGC	2158
QY	2416	AGGAGCAACCCCTGTGATGATTACGACTACATGGAGAAAGGCAACGCAACGAGTTCC	2475
Db	2159	AGGAGCAACCCCTGTGATGATTACGACTACATGGAGAAAGGCAACGCAACGAGTTCC	2218
QY	2476	TCAGTCCCAACAGCTGGAGAGACAGCGAGGGGCGCCTGGGAGCGGAGGCTG	2535

Db 317 TGTTCACAGAGAGAGAGTACTTGCAGTGTACTAACAAGACTGCACCTGCTGCTC 376
QY 616 TGTGGGACACCCAGGAGAGGATGCCGGGGGSCCTGGGGAAGAAGTCTCCCGGAGCTAC 675
Db 377 TGTGGGACACCCAGGAGAGGATGCCGGGGGSCCTGGGGAAGAAGTCTCCCGGAGCTAC 436
QY 676 GGTCTGCTTACTCCCGGAGATGTGCGCGCTGTGATGGCTTGGAAGACCGCTGGGGTCAAG 735
Db 437 GGTCTGCTTACTCCCGGAGATGTGCGCGCTGTGATGGCTTGGAAGACCGCTGGGGTCAAG 496
QY 736 AGGTGATCTACAGCAATGAGAGACCTTAGGGAGTGTGCTGTAAGAACCTTGGGCCCCCA 795
Db 497 AGGTGATCTACAGCAATGAGAGACCTTAGGGAGTGTGCTGTAAGAACCTTGGGCCCCCA 556
QY 796 TGGTTGGCCGAGCTGTGCTGCTTCTACCCCGGGGTGACCGGGGTATGAGTCTGTCTGC 855
Db 557 TGGTTGGCCGAGCTGTGCTGCTTCTACCCCGGGGTGACCGGGGTATGAGTCTGTCTGC 616
QY 856 GGGTAGAGCTATAGTGTGCTGTGAGGAGTGTGCTGTCTTACACCGCGCTGTGC 915
Db 617 GGGTAGAGCTATAGTGTGCTGTGAGGAGTGTGCTGTCTTACACCGCGCTGTGC 676
QY 916 GGCAGACAAATGTATTTATCTGAGGCGGTGTACCTCAACGACTCCACCTATGACGAGACATA 975
Db 677 GGCAGACAAATGTATTTATCTGAGGCGGTGTACCTCAACGACTCCACCTATGACGAGACATA 736
QY 976 CGGTGGGCGGACGTACAGTATAGGGGGTCTGGCCACAGCTGGCAGATGTGTGTGGGGCTGG 1035
Db 737 CGGTGGGCGGACGTACAGTATAGGGGGTCTGGCCACAGCTGGCAGTATGTGTGGGGCTGG 796
QY 1036 ATGACTTTAGGAAGAGTACAGAGCTGGGGGTGTGGCCAGGCTATGACTATGTGGAGATGA 1095
Db 797 ATGACTTTAGGAAGAGTACAGAGCTGGGGGTGTGGCCAGGCTATGACTATGTGGAGATGA 856
QY 1096 GCAACACAGCTTCTCAGTGTGCTATGTGAGATGTGAGTGTGAGCTTGTGACCGGTGAGG 1155
Db 857 GCAACACAGCTTCTCAGTGTGCTATGTGAGATGTGAGTGTGAGCTTGTGACCGGTGAGG 916
QY 1156 CCTTCAGGCTATGACAGTGTGCTGCGGCGTGCCTATGCGCTGGGAGAGCCGCTGTGCTG 1215
Db 917 CCTTCAGGCTATGACAGTGTGCTGCGGCGTGCCTATGCGCTGGGAGAGCCGCTGTGCTG 976
QY 1216 GCGGGGTGAATGTGCTGCTGCGGCGTGCCTATGCGCTGGGAGAGCCGCTGTGCTG 1275
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QY 1276 GCCACAACCTAGGGGGCAACTGTGGGGAGCCCAAGAGCCCGGCTGTCTAGTACCCCTTG 1335
Db 1037 GCCACAACCTAGGGGGCAACTGTGGGGAGCCCAAGAGCCCGGCTGTCTAGTACCCCTTG 1096
QY 1336 GGGGGCTGTGCTGCTGCTTCTGCAAGTGCCTTCTCTTTGGGGGCGCTGTGACTCT 1395
Db 1097 GGGGGCTGTGCTGCTGCTTCTGCAAGTGCCTTCTCTTTGGGGGCGCTGTGACTCT 1156
QY 1396 TCAGGAATATCTCTTCACTCTGTATGTGGTGAACAATTCCTCTCCGGACTGTGGAGGA 1455
Db 1157 TCAGGAATATCTCTTCACTCTGTATGTGGTGAACAATTCCTCTCCGGACTGTGGAGGA 1216
QY 1456 CTTTCGCCAGCCCGCTGTGGGCGCTGCGCCACCTCCCAACAACCTCAGAGAGTTGG 1515
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QY 1516 AGCTGAGACCCAGAGAGCCAGAGCCGCTGTGGCCAGAGCCGAGGAGAGCCGAGCCGATCC 1575
Db 1277 AGCTGAGACCCAGAGAGCCAGAGCCGCTGTGGCCAGAGCCGAGGAGAGCCGAGCCGATCC 1336
QY 1576 TCATCGGCTGTGCTGTGGCCATTCCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1635
Db 1337 TCATCGGCTGTGCTGTGGCCATTCCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1396
QY 1636 GCGGGCTGACTGGCGAGGCTCTCTCAAGCAAGGCTGAAGGAGGAGTGTGGAGAGAGGAGC 1695
Db 1397 GCGGGCTGACTGGCGAGGCTCTCTCAAGCAAGGCTGAAGGAGGAGTGTGGAGAGAGGAGC 1456

QY 1696 TGACGGTTACCTCTCTGTCTCCCTGGGGACACTATCTCATCAACAACCGCCAGGCTCTA 1755
Db 1457 TGACGGTTACCTCTCTGTCTCCCTGGGGACACTATCTCATCAACAACCGCCAGGCTCTA 1516
QY 1756 GAGAGCCACCCCGTACCAAGAGACCCCGGCTGTGGGAATCCGCCACATCCGCTCCCT 1815
Db 1517 GAGAGCCACCCCGTACCAAGAGACCCCGGCTGTGGGAATCCGCCACATCCGCTCCCT 1576
QY 1816 GTGTCCCAATGAGGCTGTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1875
Db 1577 GTGTCCCAATGAGGCTGTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1636
QY 1876 CTTAGCCCGCTCCCTCTGAGGAGCCCGGAGCCCGCCACACCGCGCTGGGGCCAAACCCACA 1935
Db 1637 CTTAGCCCGCTCCCTCTGAGGAGCCCGGAGCCCGCCACACCGCGCTGGGGCCAAACCCACA 1696
QY 1936 ACACCCAGGCTACAGTGGGGAGTATATGAGGCTGTAGAGAGCCAGGCGCCGCTGTGC 1995
Db 1697 ACACCCAGGCTACAGTGGGGAGTATATGAGGCTGTAGAGAGCCAGGCGCCGCTGTGC 1756
QY 1996 CCCACCTCCCGCAGAAACAGGCTCCCGCATTTATGCGAGGCTGACATTTTACCTGCAGG 2055
Db 1757 CCCACCTCCCGCAGAAACAGGCTCCCGCATTTATGCGAGGCTGACATTTTACCTGCAGG 1816
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Db 1817 GCGTCACCGGGGGCAACACCTATGCTGTGCTGTGACGCGCCCGGAGGAGCTGGGGATG 1876
QY 2116 GGGCCCCCAGAGTGTATTCCTCTGATCTGACTCCGCTTCAAGAGAACTTGGGAGG 2175
Db 1877 GGGCCCCCAGAGTGTATTCCTCTGATCTGACTCCGCTTCAAGAGAACTTGGGAGG 1936
QY 2176 GCCAGTTGGGGAGAGTGCACCTGTGTAGGTGCAGACGCTCAAGATCTGTGCTGCTG 2235
Db 1937 GCCAGTTGGGGAGAGTGCACCTGTGTAGGTGCAGACGCTCAAGATCTGTGCTGCTG 1996
QY 2236 ATTTCCCGCTTAATGTGCTGAAGGAGACGCTTGTGCTGTGATGTCAAAATCTTACGCG 2295
Db 1997 ATTTCCCGCTTAATGTGCTGAAGGAGACGCTTGTGCTGTGATGTCAAAATCTTACGCG 2056
QY 2296 CAGATGCCACCAAGAAATGCGAGCTTCTCTTCTCCAGAGATGATTTCTGAAAGAG 2355
Db 2057 CAGATGCCACCAAGAAATG-----CAGAGATGATTTCTGAAAGAG 2098
QY 2356 TGAAGATCATGTGAGGCTCAAGAGCCCAACATCTGCGCTGTGGGCTGTGTGC 2415
Db 2099 TGAAGATCATGTGAGGCTCAAGAGCCCAACATCTGCGCTGTGGGCTGTGTGC 2158
QY 2416 AGGAGACCCCGCTGTGATGATTAAGTACGACTACATGTGAGAGAGCGGACCTCAACAATTC 2475
Db 2159 AGGAGACCCCGCTGTGATGATTAAGTACGACTACATGTGAGAGAGCGGACCTCAACAATTC 2218
QY 2476 TCAGTCCCAACAGCTGAGAGCAAGGACGAGGAGGCGCCCTGGGAGCGGGCAGGCTG 2535
Db 2219 TCAGTCCCAACAGCTGAGAGCAAGGACGAGGAGGCGCCCTGGGAGCGGGCAGGCTG 2278
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Db 2279 CGAGGGGCGCCACATCACTACCTCAATGCTGTGATGTGGAGCCAGATGCGCTCCG 2338
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2519 AGTCATCCATGAGGAGAGTTCAGACTGAGTGAAGTGGGCTTTGGTGTGACC 2578
2836 TGTGGAGAGTGTCTGATCTGTAGGGCCAGCCCTTTGGGACGCTACCGAGAGAGG 2895
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2699 CGCTGCTCCCGCAGAGGCTATATAGCTGATGCTGCTGCTGGAGCCGGAGTCTG 2758
3016 AGCAGGACGACCTTTTCCAGTGCATGAGTTCCTGGAGAGAGTACCTACACGG 3075
2759 AGCAGGACGACCTTTTCCAGTGCATGAGTTCCTGGAGAGAGTACCTACACGG 2818
3076 TGTGAATCACAATCCAGTGCCTCCCTCAGGAGTGTATCCAGGGAGAGCCAGTGACA 3135
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3376 AAGGTGGGAGAAATATAGATAGACATGAGATGAGATGAGATGAGATGAGATGAG 3435
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DEFINITION Sequence 3 from patent US 6096527.
ACCESSION AR105288
VERSION AR105288.1 GI:12818885
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3637)
AUTHORS Godowski, P., J., Mark, M., R., and Scadden, D., T.
TITLE Nucleic acids encoding protein tyrosine kinases
JOURNAL Patent: US 6096527-A 3 01-AUG-2000;
FEATURES
Location/Qualifiers
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Query Match 87.1%; Score 3451; DB 6; Length 3637;
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OY	856	GGGTAGACCTCATATGGCGCCCTCTGGAGGATGAGACTCTGTCTTACACCCGCCCTGTGG	915
Db	617	GGGTAGACCTCATATGGCGCCCTCTGGAGGAGGAGGACTCCTGTCTTACACCCGCCCTGTGG	676
OY	916	GGCAGACAATATATTTATCTGTGAGGCGCGTGTACTTCAAGACATCCACCTATGACGGACATA	975
Db	677	GGCAGACAATATATTTATCTGTGAGGCGCGTGTACTTCAAGACATCCACCTATGACGGACATA	736
OY	976	CCGTGGGCGGAGCTGCAGTATGAGGGGCTGTGGGCACTGGCAGATGATGTGTGTGGGACTGG	1031
Db	737	CCGTGGGCGGAGCTGCAGTATGAGGGGCTGTGGGCACTGGCAGATGATGTGTGTGGGACTGG	796
OY	1036	ATGACTTTAGAAAGATAGAGAGCTGCCGGTCTGTGGCAAGGCTATGATGTGTGGATGGA	1099
Db	797	ATGACTTTAGAAAGATAGAGAGCTGCCGGTCTGTGGCAAGGCTATGATGTGTGGATGGA	856
OY	1096	GCAACCAACAGCTTCTCCAGTGGCTATGTGGAGATGAGATGGAATTTGATTTACCCGGTGAGGG	1155
Db	857	GCAACCAACAGCTTCTCCAGTGGCTATGTGGAGATGAGATGGAATTTGATTTACCCGGTGAGGG	916
OY	1156	CCTTCCAGGCTATGACAGTCCACTGATTAACAACATGCAACAGCTGGAGAGCCCGCTGTCCGG	1211
Db	917	CCTTCCAGGCTATGACAGTCCACTGATTAACAACATGCAACAGCTGGAGAGCCCGCTGTCCGG	976
OY	1216	GGGGGGTGGAAATGTCCGCTTCCGGCGTGCCCTGCCATGTGCTGGGAGGGGAGCCCATGC	1277
Db	977	GGGGGGTGGAAATGTCCGCTTCCGGCGTGCCCTGCCATGTGCTGGGAGGGGAGCCCATGC	1036
OY	1276	GCCCAACCTATAGGGGGGCAACCTGGGGGAGCCCAAGAGCCCGGGGCTGTCTAGTCCCTTGG	1337
Db	1037	GCCCAACCTATAGGGGGGCAACCTGGGGGAGCCCAAGAGCCCGGGGCTGTCTAGTCCCTTGG	1096
OY	1336	GCGGCGGTGTGGCTGCGCTTCTGCAAGTGCACGCTTCTTTGGGGGGCGCTGGTACTACT	1397
Db	1097	GCGGCGGTGTGGCTGCGCTTCTGCAAGTGCACGCTTCTTTGGGGGGCGCTGGTACTACT	1156
OY	1396	TCAAGCAAAATCTCTTATCTGTGATGTGTGAACAATTCCTCTCCGACACTGGAGAGCA	1455
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OY	1456	CCATCCCGGCAAGCCCCCTGGGGGCGCGCTGGCCCAACTCCCACTTCAGACAGCTTGG	1515
Db	1217	CCATCCCGGCAAGCCCCCTGGGGGCGCGCTGGCCCAACTCCCACTTCAGACAGCTTGG	1276
OY	1516	AGCTGAGGCCAGAGGCGCAGAGCCCGCTGGGCAAGGCGGAGGGAGCCGACCGCATATCC	1577
Db	1277	AGCTGAGGCCAGAGGCGCAGAGCCCGCTGGGCAAGGCGGAGGGAGCCGACCGCATATCC	1336
OY	1576	TCAATGGCTCGCTGTGTGGCCATATCCTGTCTGCTGATCATATTGGCCTCATGTCTCT	1637
Db	1337	TCAATGGCTCGCTGTGTGGCCATATCCTGTCTGCTGATCATATTGGCCTCATGTCTCT	1396
OY	1636	GGGGGCTGCATGCGGCAAGGCTCTCTAGCAAGGCTGAACGAGAGGCTTGGAAAGAGAGC	1699
Db	1397	GGGGGCTGCATGCGGCAAGGCTCTCTAGCAAGGCTGAACGAGAGGCTTGGAAAGAGAGC	1456
OY	1696	TGACGGTTTACACTCTGTCTCCCTGGGGAGCACTATCCATATCAACAACCGCCAGTCTCTA	1755
Db	1457	TGACGGTTTACACTCTGTCTCCCTGGGGAGCACTATCCATATCAACAACCGCCAGTCTCTA	1516
OY	1756	GAGAGCCACCCCGTATGACAGAGAGCCCGGCTGTGTGGAAATCCGCCCCACTCCGCTCCCT	1815
Db	1517	GAGAGCCACCCCGTATGACAGAGAGCCCGGCTGTGTGGAAATCCGCCCCACTCCGCTCCCT	1576
OY	1816	GGTGTCCCAATGGCTGTGGGTGTGTCTCTCCATATCCAGCTTACCGGCTCTTCTTGAGCA	1875
Db	1577	GGTGTCCCAATGGCTGTGGGTGTGTCTCTCCATATCCAGCTTACCGGCTCTTCTTGAGCA	1636
OY	1876	CTTACGCGCCGCTCCCTCTGAGGGGCGGGGCGCCCAACCGGCTGGGCGCAACCCAGCA	1935
Db	1637	CTTACGCGCCGCTCCCTCTGAGGGGCGGGGCGCCCAACCGGCTGGGCGCAACCCAGCA	1696
OY	1936	ACACCCAGGCTCATAGTGGGAGCTATATGAGAGCTTATGAGAGCCAGGCGCCCGCTTCTGCG	1995

Db	1697	ACACCAGGCGCTACAGTGGGGAGCTTATAGAGGCGCTGAGAAAGCCAGGCGCCCGCTTCTGC	1750
Qy	1996	CCCCACTTCCCCAGAAACAGCGTCCGCCATTTATGCGGAGGCTGCAATTGTTACCTGCAG	2055
Db	1757	CCCCACTCTCCCGAAGAACAGCGCCGCCCTTTATGCGGAGGCTGCAATTGTTACCTGCAG	1811
Qy	2056	GGGTACCGGGGGGCAACACTATGCTGTGCTGCACACTGCCCCAGGGGCGAGTGGGGATG	2116
Db	1817	GGGTACCGGGGGGCAACACTATGCTGTGCTGCACACTGCCCCAGGGGCGAGTGGGGATG	1876
Qy	2116	GGCCCCCAGAGTGGATTTCCTCGATGTGCATCCGCTTCAAGGAAAGCTGGGGAG	2175
Db	1877	GGCCCCCAGAGTGGATTTCCTCGATGTGCATCCGCTTCAAGGAAAGCTGGGGAG	1933
Qy	2176	GCCAGTTTGGGGAGGTGCACCTGTGTGAGGTGCAGACCCCTCAAGATCTGTGACTGTG	2233
Db	1937	GCCAGTTTGGGGAGGTGCACCTGTGTGAGGTGCAGACCCCTCAAGATCTGTGACTGTG	1996
Qy	2236	ATTTTCCCCCTTAATGTGGGTAAAGGACACCTTTGCTGTGATGTGTCAAGATCTTAAGCG	2296
Db	1997	ATTTTCCCCCTTAATGTGGGTAAAGGACACCTTTGCTGTGATGTGTCAAGATCTTAAGCG	2055
Qy	2296	CAGATGCCAACCAAGATGCCAGCTTCCTCCTGTCTCCAGAGATGATTTTCCTGAAGAG	2355
Db	2057	CAGATGCCAACCAAGATG-----CAGAGATGATTTCTGAAGAG	2096
Qy	2356	TGAAGATCATGTGAGGCTCAAGAGCCCAACATCATTCGCGTGCAGGCGTGTGTGTG	2415
Db	2099	TGAAGATCATGTGAGGCTCAAGAGCCCAACATCATTCGCGTGCAGGCGTGTGTGTG	2155
Qy	2416	AGGACGAGCCCTCTGCATGATTTACTACTATCATGAGAAAGCGCATCTAACAGTTCC	2475
Db	2159	AGGACGAGCCCTCTGCATGATTTACTACTATCATGAGAAAGCGCATCTAACAGTTCC	2218
Qy	2476	TGAGTGCCACAGCTGGAGGACAAAGGACCCAGAGGGGCCCTGGGGAGCGGGCAGGCTG	2533
Db	2219	TGAGTGCCACAGCTGGAGGACAAAGGACCCAGAGGGGCCCTGGGGAGCGGGCAGGCTG	2278
Qy	2536	CGCAGGGGCCCAACATCAGCTACCCCAATGCTGTGCATGTGAGGAGCCGAGTCCGCTCG	2595
Db	2279	CGCAGGGGCCCAACATCAGCTACCCCAATGCTGTGCATGTGAGGAGCCGAGTCCGCTCG	2338
Qy	2596	GCATCGCTATCTGGGCCACACTCACTTTGTATCGGAGCCTGGCCAGCGCGGAATGCC	2655
Db	2339	GCATCGCTATCTGGGCCACACTCACTTTGTATCGGAGCCTGGCCAGCGCGGAATGCC	2398
Qy	2656	TAGTTGGGGAAATTTCAACATCAAAATGCCAATCTTGGCATGAGCCGGAACCTCTATG	2715
Db	2399	TAGTTGGGGAAATTTCAACATCAAAATGCCAATCTTGGCATGAGCCGGAACCTCTATG	2458
Qy	2716	CTGGGAGATTATTAACCTGTGTGAGAGGGCGGGCAGTGTGCCATTCGCGGTGAATGGCTGG	2775
Db	2459	CTGGGAGATTATTAACCTGTGTGAGAGGGCGGGCAGTGTGCCATTCGCGGTGAATGGCTGG	2518
Qy	2776	AGTGCATCTCATGSGGGAAGTTCAAGCACTGCGAGTACGTGTGGGCTTTGTGTGACCC	2835
Db	2519	AGTGCATCTCATGSGGGAAGTTCAAGCACTGCGAGTACGTGTGGGCTTTGTGTGACCC	2578
Qy	2836	TGTGGAGGTGTCTATGCTTGTAAAGGCCAGCCCTTTGGGAGGCTCAACGAGCAGG	2895
Db	2579	TGTGGAGGTGTCTATGCTTGTAAAGGCCAGCCCTTTGGGAGGCTCAACGAGCAGG	2638
Qy	2896	TCATCGAAGAACGGGGGGAATTTCTCCGGGACCAAGGCGCGGAGTGTACTGTCCGGC	2955
Db	2639	TCATCGAAGAACGGGGGGAATTTCTCCGGGACCAAGGCGCGGAGTGTACTGTCCGGC	2698
Qy	2956	CGCCTGCTCTCCCGCAGGGGCTTATGAGCTATGCTTCGAGGTGTGGAGCGCGGAGTGTG	3015
Db	2699	CGCCTGCTCTCCCGCAGGGGCTTATGAGCTATGCTTCGAGGTGTGGAGCGCGGAGTGTG	2758
Qy	3016	AGCAGGACACCCCTTTCCCACTGTCATCGGTTCTGTGGCAGAGATGCACCTCAACAGG	3075

Db	857	GCACACACAGCTTCTCCAGTGGCTATGTGAGAGTAGCACTTTGAGTTTGACCGGCTGAGAGG	916
OY	1156	CCTTCCAGGCTATGCAAGGTCCACTGTAAACAACATGCACACGCTGGGAGCCCGTTCGGCG	12115
Db	917	CCTTCCAGGCTATGAGAGGTCCACGTGTAAACAACATGCACACGCTGGGAGCCCGTTCGGCG	976
OY	1216	CGGGGGTGGAAATGTGCTTCCGGGCGTGGCCCTGCCATGGCCCTGGGAGGGGAGCCCATGCG	1277
Db	977	CGGGGGTGGAAATGTGCTTCCGGGCGTGGCCCTGCCATGGCCCTGGGAGGGGAGCCCATGCG	1036
OY	1276	GCACAACCTTGGGGGGCAACCTGGGGGAGCCCAAGAGCCCGGGGTGTCTCAGTGGCCCTTG	1335
Db	1037	GCACAACCTTGGGGGGCAACCTGGGGGAGCCCAAGAGCCCGGGGTGTCTCAGTGGCCCTTG	1098
OY	1336	CGGCGCGTGTGGGCTGCGCTTCTGAGTGGCCCTTCTTTGGGGGGCGCGGTACTCT	1399
Db	1097	CGGCGCGTGTGGGCTGCGCTTCTGAGTGGCCCTTCTTTGGGGGGCGCGGTACTCT	1156
OY	1396	TCAAGCAATCTCCTTCATCTCTGATGTGGTGAACAATTCCTCTCCGCACTGGGAGACA	1455
Db	1157	TCAAGCAATCTCCTTCATCTCTGATGTGGTGAACAATTCCTCTCCGCACTGGGAGACA	1216
OY	1456	CGTTCCCGGCAAGCCCGCTGGTGGGCGCCCTGGCCACCTCCACCAACTTGACAGCTTGG	1515
Db	1217	CGTTCCCGGCAAGCCCGCTGGTGGGCGCCCTGGCCACCTCCACCAACTTGACAGCTTGG	1276
OY	1516	AGCTGAGGCCAGAGGCGCAGAGCCGCTGGGCAAGGGCGAGGGAGGCCCGACCCCATCC	1575
Db	1277	AGCTGAGGCCAGAGGCGCAGAGCCGCTGGGCAAGGGCGAGGGAGGCCCGACCCCATCC	1336
OY	1576	TCAATGGGCTCCGTGGTGGCCATCATCCTGTGCTCGCTCATATGATGGCCCTCATGTCCT	1635
Db	1337	TCAATGGGCTCCGTGGTGGCCATCATCCTGTGCTCGCTCATATGATGGCCCTCATGTCCT	1336
OY	1636	GGGGGCTGCACTGGGCGGAGGCTCCTCAGCAAGGCTGACGAGGAGGTTGGAGAGGAGC	1695
Db	1397	GGGGGCTGCACTGGGCGGAGGCTCCTCAGCAAGGCTGACGAGGAGGTTGGAGAGGAGC	1456
OY	1696	TGACGGTTCACCTCTGTCCTCGGGGGACATATCCATCAACACACCGCCAGAGTCTCTA	1755
Db	1457	TGACGGTTCACCTCTGTCCTCGGGGGACATATCCATCAACACACCGCCAGAGTCTCTA	1516
OY	1756	GAGAGCCACCCCGCTACAGAGAGCCCGGCGCTGTGGGAATCCGCCCATCCGACTCCCT	1815
Db	1517	GAGAGCCACCCCGCTACAGAGAGCCCGGCGCTGTGGGAATCCGCCCATCCGACTCCCT	1576
OY	1816	GTGTCCCCCAATGGCTGTGCTGTCTGCTCTCAATCCAGGCTTACCGGCTCTTGTGGCA	1875
Db	1577	GTGTCCCCCAATGGCTGTGCTGTCTGCTCTCAATCCAGGCTTACCGGCTCTTGTGGCA	1696
OY	1876	CTTACGCCCGTCCCGCTCGAGGCGCGGGGCCCGCAACCCGCGCTGGGCCAAACCCACCA	1935
Db	1637	CTTACGCCCGTCCCGCTCGAGGCGCGGGGCCCGCAACCCGCGCTGGGCCAAACCCACCA	1696
OY	1936	ACACCCAGGCTCAAGTGGGAGATATATGAGAGCTAGAGAGCCAGGCGCCCGCTTCTGC	1995
Db	1697	ACACCCAGGCTCAAGTGGGAGATATATGAGAGCTAGAGAGCCAGGCGCCCGCTTCTGC	1756
OY	1996	CGCCACCTCCCGCAGAACACAGCTGCCCATTTATGCGCAGAGGCTGACATTTGTTACCTCTCAG	2055
Db	1757	CGCCACCTCCCGCAGAACACAGCTGCCCATTTATGCGCAGAGGCTGACATTTGTTACCTCTCAG	1816
OY	2056	CGCTCACCGGGGGCAACACCTATATGCTGTGCTGCTGATGGCCCCAGGGGGAGTGGGGAGT	2115
Db	1817	CGCTCACCGGGGGCAACACCTATATGCTGTGCTGCTGATGGCCCCAGGGGGAGTGGGGAGT	1876
OY	2116	GGCCCCCAGATGATTTTCCCTCGATCTGCACTCGGCTTCAAGAGAGATGTCGGAGG	2175
Db	1877	GGCCCCCAGATGATTTTCCCTCGATCTGCACTCGGCTTCAAGAGAGATGTCGGAGG	1936
OY	2176	GCCAGTTTGGGAGGAGGCAACGTGTGAGAGGTGACAGCCCTCAAGATGTGTGATGCTTG	2235
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QY	2236	ATATCCCCCTTAATGTGGGTAAAGGACACCTTGTCTGGTATGCTGTCAAGATCTTAAGGC	2299
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QY	2296	CAGATGCCACCAAGAAATGCGACAGCTTCTCCTGTTCACAGAAATGATTCCTGAAGAAG	2356
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QY	2536	CCGAGGGGCCACCATCAGTACCAACCAATGGTGGCATATGGAGAGCCAGATCGCTCCG	2596
Db	2279	CCGAGGGGCCACCATCAGTACCAACCAATGGTGGCATATGGAGAGCCAGATCGCTCCG	2338
QY	2596	GCATCGCTATCTGGCCACATCAACTTTGTATCGAGACCTGGCGACGCGGAACTGCG	2656
Db	2339	GCATCGCTATCTGGCCACATCAACTTTGTATCGAGACCTGGCGACGCGGAACTGCG	2398
QY	2656	TGCTTGGGAAAAATTCACATCAAAATCGCAGACTTTGGCATGAGCCGGAACCTCTATG	2715
Db	2399	TGCTTGGGAAAAATTCACATCAAAATCGCAGACTTTGGCATGAGCCGGAACCTCTATG	2458
QY	2716	CGGGGACTATTACCGTGTGAGGGCGCGGGCATGCTGCCCATCCGCTGGATGCGCTGG	2775
Db	2459	CTGGGACTATTACCGTGTGAGGGCGCGGGCATGCTGCCCATCCGCTGGATGCGCTGG	2518
QY	2776	AGTGCATCTTATGGGGAAGTTCACGACTCGAGTACAGTGGGGCTTTGGTGTGACCC	2835
Db	2519	AGTGCATCTTATGGGGAAGTTCACGACTCGAGTACAGTGGGGCTTTGGTGTGACCC	2578
QY	2836	TGTGGAGTCTGATGCTGTGTAAGGGCCAGCCCTTTGGGAGGCTCAACGACAGCAGG	2895
Db	2579	TGTGGAGTCTGATGCTGTGTAAGGGCCAGCCCTTTGGGAGGCTCAACGACAGCAGG	2638
QY	2896	TCATCGAAGAAAGCGGGGGAATCTTCCGGGACCAAGGGCGGAGGTATCCTGTCCGGC	2955
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QY	2956	CGCGCTGCGCCGACAGGGCTTATATGAGTGTATGTTGGGAGCGGAGCGGAGTGTG	3015
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QY	3256	CCCTTCTGGACACACTCTCATGTCCCCCTTCTGTCTTCTCTTGAAGGCCCTGTGCG	3315
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OY	3316	CCACACCAGCTGGTCTGTGGATGGGAAATCCTTCACACCTCTCTAGCATCCCTTTGGGG	3375
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Dd	3033	AAGGCTGGGGAATAATATAGATTAGACACTGCATCGGCCATTTGGAGCACTGGGGCCC	3092
OY	3436	ACTGCACAACACTGATTTCCCTGGAGAGGTGCTGGC-CCCCAGCTTCTCTCCCTGTCA	3494
Dd	3093	ACTGCACAACACTGATTTCCCTGGAGAGGTGCTGGC-CCCCAGCTTCTCTCCCTGTCA	3152
OY	3495	ACACTGGACCCACAGGCTTGANAATCTGGGGGTGAGGAGAACAAAGAGAGAAAAAG	3554
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OY	3615	GAAACACTGGACCTGGGGGTAGCCCCGCCGCCAGCCTCAGTCACCCCCACTTCCACTTG	3674
Dd	3273	GAAACACTGGACCTGGGGGTAGCCCCGCCGCCAGCCTCAGTCACCCCCACTTCCACTTG	3332
OY	3675	CAGTCTTGAGCTAATAACTCTCTCTAAGCTTACGCTTTCTCTGGAGATAATTTGGATT	3734
Dd	3333	CAGTCTTGAGCTAATAACTCTCTCTAAGCTTACGCTTTCTCTGGAGATAATTTGGATT	3392
OY	3735	GGGGGAAAAGAGGAGCAACAGCGCCATAGCCTTGGGGGTGAGCATCTCTAGTAGCTGC	3794
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 3554)		
JOURNAL	Di Marco, E., Cutuli, N., Guerra, L., Canceda, R. and De Luca, M.		
MEDLINE	Molecular cloning of trke, a novel trk-related putative tyrosine		
REFERENCE	kinase receptor isolated from normal human keratinocytes and widely		
AUTHORS	expressed by normal human tissues		
TITLE	J. Biol. Chem. 268 (32), 24290-24295 (1993)		
JOURNAL	De Luca, M.		
MEDLINE	2 (bases 1 to 3554)		
REFERENCE	Direct Submission		
AUTHORS	Submitted (08-SEP-1993) M. De Luca, Istituto Nazionale per la		
TITLE	Ricerca sul Cancro, Lab Differenziamento Cellulare, Viale		
JOURNAL	Benedetto XV, 10 - 16132 Genova, ITALY		
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QY	457	ACATCTCTGCTTCCAGCTCTCTGTGATGATTTCCACTGCGCCCGCCACAGACAGATTGAGA	516
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DEFINITION H.sapiens EDDRI gene for receptor tyrosine kinase.
ACCESSION Z29093
VERSION Z29093.1 GI:732799
KEYWORDS receptor tyrosine kinase.
SOURCE human.

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ORGANISM Homo sapiens
REFERENCE Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 3841)
Laval, S., Butler, R., Shelling, A.N., Hanby, A.M., Poulsen, R. and
Ganesan, T.S.
TITLE Isolation and characterization of an epithelial-specific receptor
JOURNAL tyrosine kinase from an ovarian cancer cell line
MEDLINE Cell Growth Differ. 5 (11), 1173-1183 (1994)
95151638
REFERENCE 2 (bases 1 to 3841)
AUTHORS Shelling, A.N., Butler, R., Jones, T., Laval, S., Boyle, J.M. and
Ganesan, T.S.
TITLE Localization of an epithelial-specific receptor kinase (EDDR1) to
JOURNAL chromosome 6q16
MEDLINE Genomics 25 (2), 584-587 (1995)
95309932
REFERENCE 3 (bases 1 to 3841)
AUTHORS Kedingner, C.
TITLE Direct Submision
JOURNAL Submitted (17-DEC-1993) Claude Kedingner, CNRS Laboratoire de
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Query Match 85.0% Score 3366: DB 9: Length 3841:
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OY 2437 TTACTGACTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2496
Db 2324 TTACTGACTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2383
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Db	2384	ACAAAGCAGCGCAGAGGGGGCCCCCTGGGGACGGGACGAGCTCCGACAGGGGCCACACATCAACT	2443
0Y	2357	ACCCAAATGCTGCTCAATGTGGACAGCCAGATGCGCTCCGGCATGCGCATCTGTGGCTCAAC	2616
Db	2444	ACCCAAATGCTGCTCAATGTGGACAGCCAAATGCGCTCCGGCATGCGCTATCTGGCTCAAC	2503
0Y	2617	TCAAACTTGTACATCGGAGACTGGGCCACGCGGAATGCTCCTAATTGGGAAAAATTTCACCA	2676
Db	2504	TCAACTTGTGTACATCGGAGACTGGGCCACGCGGAATGCTCCTAATTGGGAAAAATTTCACCA	2563
0Y	2677	TCAAAATCGCAGACTTTGGCATATAGCCCGGAACCTCTATCTCTGGGGAATTAACGTGTGC	2786
Db	2564	TCAAAATCGCAGACTTTGGCATATAGCGAAGCTCTATCTCTGGGGAATTAACGTGTGC	2623
0Y	2737	AGGGCCGGGAGAGTGTCCCATCCGCTGGATGGCCCGGGAGTGCATCTCATGGGGAAGT	2786
Db	2624	AGGGCCGGGAGAGTGTCCCATCCGCTGGATGGCCCTGGGAGTGCATCTCATGGGGAAGT	2683
0Y	2797	TCACGACTGCGAGTGAACGTGTGGGCTTTTGGTGTACCTGTGGAGGGTGTGTATGCTCT	2856
Db	2684	TCACGACTGCGAGTGAACGTGTGGGCTTTTGGTGTACCTGTGGAGGGTGTGTATGCTCT	2743
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Db	2744	GTAGGGGCCAGGCCCTTTGGGCAACCTACCGACAGACAGTTCATCGAAGACCGGGGAGT	2803
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Db	2804	TCTTCCCGGACACAGGGCCGCGAGGTATACCTCTCCGCGCGCTCTCTGCCGACAGGGCC	2883
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Db	2864	TATATGACTGATGCTTCGGTCTGTGGAGCCGCGGAGTCTGTAGCGAGCACACCTTTTCC	2923
0Y	3037	AGCTGCACTCGGTTCTCGGGACAGAGATGACCTAACACGGTGTGAATCTACACATCCAGTG	3096
Db	2924	AGCTGCACTCGGTTCTCGGGACAGAGATGACCTAACACGGTGTGAATCTACACATCCAGTG	2983
0Y	3097	CCCCCTCCCTCAGGAGATGATCCAGGGGGAAGCCAGTGACACTAAACAAGAGACACAATG	3156
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Db	3164	TGTCCCTTCTGTCTTCTTCTTCTTCTAGAGCCCCCTGTGCGCCACCCAGCTGTCTGT	3223
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Db	3284	GGATAGACATGACATGAGCCATTGGAGACATCTGGGCCCACTGGAACAACTGATTC	3343
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Db	3344	TGAGAGAGTGGCTGC - CCCCAGCTTCTCTCTCTCTCTCTACACACTGAGCCCACTGGCT	3403
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OY	3814	TCACCTGGGGTTGTGTACATTTTGGGGGAGAGACACAGATTTTACACTAATATATGA	3873
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Db	3824	CCACAAAAAAAAAAAAA 3841	

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LOCUS	3692 bp mRNA PRI 31-JUL-1996
DEFINITION	Homo sapiens Cak receptor kinase mRNA, complete cds.
VERSION	L57508
KEYWORDS	GI:1160924
SOURCE	receptor kinase. Homo sapiens lung cDNA to mRNA.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE	1 (bases 1 to 3692) Perez,J.L., Jing,S.O. and Wong,T.W. Identification of two isoforms of the Cak receptor kinase that are coexpressed in breast tumor cell lines Oncogene 12 (7), 1469-1477 (1996)
JOURNAL MEDLINE	96204002
FEATURES	Location/Qualifiers 1..3692 <code>/organism="Homo sapiens"</code> <code>/db_xref="taxon:9606"</code> <code>/tissue_type="lung"</code> <code>/note="(vector lambda gt10)"</code> 193..2823 <code>/gene="Cak"</code> 193..2823 <code>/gene="Cak"</code> <code>/codon_start=1</code> <code>/product="receptor kinase"</code> <code>/protein_id="AAB05208.1"</code> <code>/db_xref="GI:1160925"</code> translation="MGPEALSLILLILIVASGDAMKHPAPAKRYALGMDRTIP SDISASSWDSSTAAHRSLRLESSDGGDAKMCAGSVFPRREXYLOYDIQRLHLVALVGT QGRIRAGLGKEFSRSYLRYSRDGRMMGNDRNGOEYISGENDEGVVLDDGPIM ARLRFYPRADRVMSVCLRELVELGLMRDGLISTAPVGOTMYLSEAVYLNDSTDYDG TVGGLQYGGLADLVADVGLDFPKRSOELRWMPDYVGWSNHSFGYVMEEFPDR LRFAQAOVHCNNMHITLGARLPGECEFRFGPMAMGEPNRHNLSGNLDPPARA SVPLSGVARFLDQCRLFAGMPLFESETSFSDVNNSPALGTFPPAPAMPWPDPPE TNSGLELEPRGOOPVAKAGESPAILIGICLVAIILLILIALMLRHRRLLSKRA ERYRIEELTYVHLSVPGDITLINRKPREPPRPQEPBRPNPHSNACPYANGCASYS DMYPERFPGAPILPPEPPONSYPHRLAEADITYLOSVTAGNTAYPALEPGAAGDP DFPSRTRFERKUGEGOFGEVHLCEVSPDLVSDPFLYNKRKPLILVAVKITPD TKARNQLFKVEKJITMSRLKDPIIIRLAGVCVODDPLCIIDYMENGDLNFLSAHQEE DKAAEGAPGGGOAAOGPTISYPMILHVAQAIAQSMRYLATLVENRDLATFNCLVGER
CDS	gene

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 AF026259 3659 bp mRNA 26-OCT-1997
 LOCUS Mus musculus receptor-like tyrosine kinase (Nep) mRNA, complete
 DEFINITION cds.
 ACCESSION AF026259
 VERSION AF026259.1 GI:2564939
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 3659)
 AUTHORS Zerlin, M., Julius, M.A. and Goldfarb, M.
 TITLE NEP: a novel receptor-like tyrosine kinase expressed in
 proliferating neuroepithelia
 JOURNAL Oncogene 8 (10), 2731-2739 (1993)
 MEDLINE 9330947
 REFERENCE 2 (bases 1 to 3659)
 AUTHORS Zerlin, M., Julius, M.A. and Goldfarb, M.

Db 1425 GCGGCTGCTCAGCAAGGCTGACAGCGCGTGTGGAGGAGAGCTGACGGTACCTTT 1484
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DEFINITION	Mus musculus Cak receptor kinase mRNA, complete cds.		31-JUL-1996
ACCESSION	L57509		
VERSION	L57509.1	GI:1161062	
KEYWORDS	receptor kinase.		
SOURCE	Mus musculus (strain C57BL)	CDNA to mRNA.	
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 3674)		
TITLE	Perez, J.L., Jing, S.O. and Wong, T.W.		
JOURNAL	Identification of two isoforms of the Cak receptor kinase that are coexpressed in breast tumor cell lines		
MEDLINE	Oncogene 12 (7), 1469-1477 (1996)		
FEATURES	96204002		
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BASE COUNT	721 a	1090 c	1079 g
ORIGIN			784 t
Query Match	60.0%	Score 2378.4	DB 10; Length 3674;
Best Local Similarity	81.3%	Pred. No. 0;	
Matches 2981;	Conservative 0;	Mismatches 581;	Indels 104; Gaps 15;
QY	277	AGAGATGCTGCCACCCCTTAGGCGCCGAGGATCAGAGATATGGACACAGAGCC	336
Db	63	AGAGATGCTGCCACCCCTTAGGCGCCGAGGATCAGAGATATGGACACAGAGCC	122
QY	337	TGCTATCTTTACTGCTG--CTCTTGTTGGCAAGTGAATGCTGACATGAAGGAC	393

Db	123	TCATCTCTCTACTGCTGTGCTGCTACTCTGTGGACAAATTGGAGATGGCATATGAAGGAC	182
QY	394	ATTTTGGATCTGCGCCAGAGTCCGGCTATGCGCTGGGCATGCAAGACCGGACCATCCAGACA	453
Db	183	ATTTTGGACCTTGTCCAAAGTGGCGGTATGCGCTGGGCATGCAAGACCGACCATCTCCAGACA	242
QY	454	GTCACATCTCTGCTTCCAGCTCTGTGTCAGATTTCATCTGGCGCGGCACAGACGGTTGG	513
Db	243	GGGATATCTGTGTGCCAGCTCTCTGTGTGGACTTACCCTGTGCCCGCCACAGACGGCTGG	302
QY	514	AGAGCATGTGACGGGGAGGGGCGTGGTCCCGCAGGGTGGATTTCCTCCAAAGAGAGG	573
Db	303	AAAGCATGTGAGAGATGGGCGCTTGGTCCCTGCAGGGCGCTGTGTTCCCAAAGAGAGG	362
QY	574	AGTACTTGCAGTGGATCTTCAAGAGATCCACCTGGTGTCTCTGTGTGGGACACCCAGGAC	633
Db	363	AGTACTTGCAGTGGACCTTCTGTAGGTCTACACCTGGTGTCTGTGTGGGACACCCAGGAC	422
QY	634	GGCATGCGGGGGGCGCTGGGCAAGAGATTCTCCGGACCTACCGGCTGCGCTTACTCCGGG	693
Db	423	GCCATGCTGGGGGGTCTGGGCAAAAGATTCTCCGAACTATCCGTTGCGTTACTCCGAG	482
QY	694	ATGTCGCGCGCTGGATGGGCTGGAAGGACCGCTGGGGTCAAGAGGTATCTCAGCGAATG	753
Db	483	ATGGCGCGCGCTGGATGGACTGGAAGGACCGCTGGGGACAGAGGTGATTTCGGGGTAAG	542
QY	754	AGGACCCGAGGAGATGGTGTGTGAAGAACCTTGGGCGCCCCCATGTTGGCCCATGCTTC	813
Db	543	AGGATCCCGGGGGAGATGGTGTGAAGGACCTTGGGCGCCCCCATGTTGGGCGCGGTGCC	602
QY	814	GCTTCTACCCCCGGGGCTGACCGGGCTCATGTAGTCTGTCTGCGGGTAGAGCTCTATGGCT	873
Db	603	GCTTCTACCCCCAGGGGCTGAACGGGTCTATGATGTCTGTCTGTGCGGTGGAGCTCTATGGCT	662
QY	874	GCTTCTGAGAGGATGAGACTCTGTCTTTACACCGCGCCCTGTGGGGCAGACATGTATTTAT	933
Db	663	GCTTCTGCGGGAGTGGACTCTGTCTCATATTCACACCCCGTGGGGGAGACATGAGTTAT	722
QY	934	CTGAG --- CCGTCTACTTCAAGACATCCACATATGACGACATACCGTGGGGGACATGCG	990
Db	723	CTGAGGTGATGTATCATCTCATATGATTTCCACTTACGATGATATATCTGTGGAGGGCTGCG	782
QY	991	AGTATGGGGGCTCTGGGCGCACTGGCAGATGCTGTGTGGGGCTGATGACTTTAGAGA	1050
Db	783	AGTATGGGGGCTCTGGGCGCACTGGCAGATGCGCTGTGGGGCTGATGATTTCAAGGAGA	842
QY	1051	GTCAGGAGCTCGGGGCTTGGCCAGCGCTATGACTATGTGGGATGGACCAACCACTCTT	1110
Db	843	GCCAGGAGCTCGGGGCTTGGCCAGCGCTATGACTATGTGGGATGGACCAATCGACCTTCC	902
QY	1111	CCAATGCTATGTGGAATAGGATTTGAGTTTACGCGCTGAGAGGGCTCCAGGCTATGCG	1170
Db	903	CCAGGGGCTACGTGGAATAGGATTTGAGTTTATGCGTTGAGAGACTTCCAGACCAATGCG	962
QY	1171	AGGTCACTATGACATCATCATCAACGCTGGGAGCCCGTGTGCTTGGCGGGGTGGAATGTC	1230
Db	963	AGGTCACTATGACATCATCATCACTCTGGGAGCCCGCTTACAGAGTGGGTGGGAATGCC	1022
QY	1231	GCTTCCGGCGGGCGCTGGCATGAGCGCTGGGAGGGGAGGCAATGCGGCCCAACCTAAGGG	1290
Db	1023	GCTTAAAAAGGGGCTCCGCGCATGGCTCTGGGAGAGAGAGCTGTCCGCAATGCTCTGGAG	1082
QY	1291	GCAACCTGGGGAGACCCAGAGACCCCGGGGCTGTCACTGCCCCCTTGGCGGCGCTGTGGCTC	1350
Db	1083	GCAACCTTGGAGACCCAGAGACCCCGGGGCATCATGATGCCCCCTGGGTGGCCACGNGGCC	1142
QY	1351	GCTTTCGAGTGGCGGCTCTCTCTTTGGCGGGGCGCGGTATCTTTCAGCAAGAAATCTCTCT	1410
Db	1143	GCTTTCGAGTGCAGAAATTCCTCTTTCGAGGTCTTGTGTTACTCTTTCAGTAAGATCTTCTT	1202
QY	1411	TCATCTCTGATGTGTGACAAATTTCTCTCCCGGCACTGGGAGGCACTCTCCGCGACGCC	1470
Db	1203	TCATCTCTGATGTGTGAGAGAGATTTCTCTCT --- GACAACTCTTCCACTTAAGCTC	1250

OY	1471	CTGGGTGGCCCGCCGGGCCACCTCCACCAACTTCAACAGCTTGGAGCTGGAGCCAGAG	1530
Db	1251	CTGGGTGGCCACCTGGGGCCCGCTCCACCAACTTCAACAGCTTGGAGCTGGAGCCCGGG	1310
OY	1531	GCCAGCAGCCGTGGCCAAAGGCGAGGGAGGCCGACCGGCATCTGATGGCGCTGG	1590
Db	1311	GTCACAGCGCATGTGGCCAAAGGCGAGGGAGGCCGACCGGCATCTGATGGCGCTGG	1370
OY	1591	TGGCCATCATCTGCTCTGCTGCTCATCTTGGCCCTCATGCTCTGGCGGCTGCATCGC	1650
Db	1371	TGGCCATCATCTGCTGCTGCTCTCATCTTGGCCCTCATGCTCTGGCGGCTGCATCGC	1430
OY	1651	GCAGGCTCCACACAGAGCGTGAACGAGGGTGTGGAAAGGAGCTGACGGTTCACCTT	1710
Db	1431	GCCGGCTGCTCACCAAGGCTGACCGCTGCTGTGGAGGAGAGCTGACCGTTCACCTT	1490
OY	1711	CTGTCCCTGGGAGCACTATCTCATCAACACCGCCAGATCTCTAGAGAGCCACCCCGT	1770
Db	1491	CTGTCCCTGGGAGCACTATCTCATCAACACCGCCAGATCTCTAGAGAGCCACCCCGT	1550
OY	1771	ACACGAGCCCGCGCTCTGGGAATCCGCCCCACTCCGCTCCCTGTGCCCAATGGCT	1830
Db	1551	ACACGAGCCCGCGCTCTGGGAGTCCACCCCATCTGTGACCCCTGGTCCCAAGGCT	1610
OY	1831	CTGCTGTGCTGCTCATCTCAACCGCTTACCGCTCTCTTGGGACTTACGCCCTGCC	1890
Db	1611	CTGCTGTGCTGCTCTCAACCGCGCTTACCGCTCTCTTGGGCACTTACGCCCTGCC	1670
OY	1891	CTTCGAGGCCCGGGCCCCCACACCGCCCTGGGCGCAACCCACCAACCCAGAGCTTACA	1950
Db	1671	CTTCGAGGCCCGGGCCCCCACACCGCGCTGGGCGCAACCCACCAACCCAGAGCTTACA	1730
OY	1951	GTGGGGACTATATGGAGCTGAGAAAGCCAGGGCCCCCGCTTGTGCCCACTGCCAGAG	2010
Db	1731	GTGGGGACTATATGGAGCCCGGAAGCCCGGGTCCCCGCTTGTACCCCACTGCCAGAG	1790
OY	2011	ACAGGCTCCCCCATTTATGGCGAGGCGTGAATGTTACCTGAGAGGGCGTACCGGGGCA	2070
Db	1791	ACAGGCTCCCCCATTTATGGCGAAGCTGCAATGTCACTCTGCAAGGCGTACCTGGGGGA	1850
OY	2071	ACACCTATCTGTGCTGCTGCACCTGCCCGCAGGGGCACTCGGGATGGGCCCGCAGATGG	2130
Db	1851	ACACCTATCTGTGCTGCTGCACCTGCCCGCAGGGGCACTCGGGATGGGCCCGCAGATGG	1910
OY	2131	ATTTCCTGATCTGCACTCCGCTTCAAGAGAAAGCTTGGCGAGGCGCAGTTGGGGAGG	2190
Db	1911	ATTTCCTGATCTGCACTCCGCTTCAAGAGAAAGCTTGGCGAGGCGCAGTTGGGGAGG	1970
OY	2191	TGCACCTGTGTAGGTGCGACAGCCCTCAAGATCTGGTCACTTATTTCCCCCTTAAG	2250
Db	1971	TACACCTGTGTAAATAGAGAGACCGCGCAAGATCTGTCACTAGTACTTCCCTATCAGG	2030
OY	2251	TGCGTAAGGAGCACCTTTGCTGTGTGATGCTGTCAAGATCTTACGGCGCAGATGCCAAGA	2310
Db	2031	TGCACAAAGGAGACCCCTGTGGGTAGAGAGTGAATCTCCGCGCAGATGCCACAAA	2090
OY	2311	ATGCCAGCTTCTCCTGTTCTTCCAGAGATGATTTCTGAAAGAGGTGAAGATCATGTGA	2370
Db	2091	ATG-----CAGGAATGATTTCTTGAAGAGGTGAAGATCATGTGAC	2132
OY	2371	GGCTCAAGGACCCCAACATCATTTGGGCTGTGGGCGTGTGTGTGAGAGCAACCCCTCT	2430
Db	2131	GGCTCAAGGACCCCAACATCATTTGGGCTGTGGGCGTGTGTGTGAGAGTGAACCCCTCT	2192
OY	2431	GCATGATTAAGTACATGAGTGAAGAAAGGCGACACCAATCTCTCAAGTGCACAGC	2490
Db	2193	GCATGATTAAGTACATGAGTGAAGAAAGGCGACATCTGAACCAATCTCTCAAGTGCACAGC	2252
OY	2491	TGGAGACAAAGGCAAGCGAGGGGGCCCTTGGGGAAGGCGCAGAGCTGCGAGGGGCCACCA	2550
Db	2253	TGGAGAACAAAGGCAACTCAGGGGGCTCTTGGGGACACAGAGATCTGACAGGGGGCCCAAA	2312

QY	2551	TCAGCATACCCATTGCTGCTGGCATGTGGCAGCCAGATGCGCTCCGGCATCGCTATCTGG	261
Db	2313	TCAGCTACCCCTTGGTGTATACAGTGGGGGGCCAGATGCGCTCTGGCATCGTATCTCG	237
QY	2611	CCACATCTCAACTTGTATGATCGGGACCTGGGACGGGAACATGCTGTTGGGAAATTT	267
Db	2373	CCACGCTGAACCTTTGTGCAATCGGACCTGGGCACCCGGAACTGTTGGTGGGAAATTT	243
QY	2671	TCACATCAAAATCGCAGACTTTGGCATGAGCCGGAACTCTATGCTGGGAGCATATACC	273
Db	2433	TCACATCAAAATTCGCCGACTTTGGCATGAGCCGGAACTCTATGAGCTGGGAGTATTAAC	249
QY	2731	GTGTGAGGGCCGGCGAGTGTGCTGCCATCCGCTGGATGGCCGTGGAGTCATCCTATGG	279
Db	2493	GTGTCCAGGGCCGGCGGCTGGCTGCCAATCAGTGGATGGCTGGAGATGCAATTCATGG	255
QY	2791	GGAGGTACGAGCTGCGAGTACAGTGTGGGCTTTGGTGTGACCTTGGAGTGTCTGA	285
Db	2553	GGAGGTACCAACAGCCAGTACGTTGGGCTTTGGAAGTACCTGTGTGGAGTGTCTGA	261
QY	2851	TGCTGTGAGGGCCGAGCCCTTTGGGAGCTCACCAGCAGCAGAGTCAATGAGAACGGG	291
Db	2613	TGCTGTGAGAGTCCAGCCCTTTGGGAGCTTACAGATGACAGTATTGACAAATGGCG	267
QY	2911	GGAGTCTTCCGGGACGAGGCGGAGAGGTACCTGTCCGGCGCGCTGCTGCCCGC	297
Db	2673	GGAGTCTTCTCAGGAGCAGGAGGCGGAGGTCATCTTGTCCAGGCCACCGCTGCCAC	273
QY	2971	AAGGCTATATGAGTATGCTTTGGGTGTGGAGCCGGGAGTGTGACAGCAGCACCTT	303
Db	2733	AACCTCTATGAGTGTATGCTTCGGGTGTGGAGCCGGGAGCCGAGCAGCGCCGCTT	279
QY	3031	TTTCCACCTGAGTGGTTCCTGGCAGAGGATGCACTCAACAGGTTGATACACATC	309
Db	2793	TGCGCCACTTCACTGCTGCTTGGCGGATGTGCTCAACAGGTTATTACTCAGAGCC	285
QY	3091	CAGTCCGCCCTCCCTCAGGAGTGTATCAGGAGGAAAGCCAGTGAACATAAACAGAGAC	315
Db	2853	CGCGAGCCCTTCCCAATGGAAAGCCATCCAGGGGAAAGTGGACTGGAATC--CAGAGA	291
QY	3151	ACAATGSACTCTGCGCTTCCCTCCCGACAGCCATCACTTAATAGAGCACTGAG	321
Db	2912	CCTAAGCCACCGCACCCACCGTCTCATCTATCTGCC--CATTCGCCAAGAGTCAATGTC	296
QY	3211	ACTGAGGTGGGCGTGGGCCACCCAGGAGCACTATGCCCTTCCCTCTGGACACA	327
Db	2970	TCTGCAAGGTTATGTGCTGGGACTGGGACTGCCAAG-----AATCAGA	301
QY	3271	CTCTCATGTCCCTCTCTGTCTTCTCTCTTAAGACCCCTGTGCGGCCACCCAGCGTGC	333
Db	3013	TTACACACACTCTTACGTTTCTTCTCTTCATGTGCAAGTGGCAACCTCCACGCTGGC	307
QY	3331	CTGTGGATGGATCTCTCCACCTCTCTTAGCCATCCTTGGGAAAGGTTGGGAGAA	339
Db	3073	CTGTGGTGGATCTCTCTGACTTCTTCCAGCTATCCCTTGGGAAAGAACGGGGCAAA	313
QY	3391	TATAGATTAAGACACTGAGCATGGCCCATTTGGAGCAGCTGGGCCCCAATGGAAACAGA	345
Db	3133	TGCTGGGCGTACACTGACAAAG-----CCCATCTGAACTTCACTGG	317
QY	3451	TTCTGAGAGAGTGGCTGCGCCACCTTCTCTCTCTCTGTCACACACTGAGACCCCATGG	351
Db	3174	TTCTCTGG--GAGGTGACGAGTGGCCCC--CGAGTTTCTTCTTGTCAACACTGAGCGCGCA	323
QY	3511	GCTAGAAATCTGGGGGTGAGGAGGACAAAGAGAGAGAAATGTTTCTCTGTGCTGCT	357
Db	3232	GCTAGAAATTAAGAGGGGTGAGGGGACAAAGAGCG-----GCCAAC	327
QY	3571	CTGTATATGTTCTCCAGCTGGGCTCTCTCTCTCTCTCATCAGCTGAACACTGGAGCTGG	363
Db	3274	CTGTACAGCGTCTCTACGCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	333
QY	3631	GGGTAGC--CCGCCCCAGGCTCACTACCCCACTTCCACTTGCAGTCTTGTAGTGA	368

Query Match	Best Local Similarity	Conservative	Score	DB	Length
Matches 3005;	81.8%;	0;	60.0%;	2378;	3743;
			Pred. No. 0;		
			Mismatches 555;	Indels 114;	Gaps 18;
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<div> <div>BASE COUNT</div> <div>ORIGIN</div> </div>					
278	GAGATGCTGCCCCCACC	CCCCCTTAGGCCCCGAGGAGTACAGAGCTATAGGACACGAGGCCCCCT	337		
135	GAGATGCTGCTCCCTCC	CTCCATGAGGCCAGAGGAGTACAGAGGATGGGAGACGAGGACCCT	194		
338	GTCATCTTACTGCTGCTG	---CTCTGGTGGCCAGAGTGGAGATGCTGACATGAGAGGACA	394		
195	CTCATCTCTCTCTGCTG	CTCTACTCTTTGGTGACATTTGGTAGATGGATGGTGCATGTGAAGGACA	254		
395	TTTGTATCTGCGCAGAG	TGCGGCTATGCCCTGGGAGTGCAGAGCCGAGACATCCGAGACAG	454		
255	TTTTATACCAGCAGAGT	GCTATGCCCCCTGGGACATGCAGACCCGACCATTCACAGACAG	314		
455	TGACATCTCTGCTTCC	AGCTCCCTGTCAGATTCACACTGCCGCCGCCACACAGAGGTTGA	514		
315	CGATATCTCTGTGTC	AGCTGCTGCTGTCGAGACTCTACGCCGCCGCCGCCACAGAGGCTGGA	374		
515	GAGCAGTACAGGGGAG	TGAGGGCCCTGGTGGCCCCGACAGGTCGGTCTTCCACAGAGGAGA	574		
375	AAGCAGTATGAGTAGT	TGGGGCTTGGTGGCTTCGACAGGGCCCTGTTCCCAAGAAGAGAGA	434		
575	GACTTGGAGGAGTAT	CTACAAACGACCTCACTGGTGGCTGCGTGGGGACACCCAGAGGACG	634		
435	GTAACCTGACAGGTGA	CACTTCGTAAGCTCACTGGTGGCTGCGTGGGGACACCCAGAGGCGC	494		
635	GCATCCCGGGGCCCT	GGGCGCAAGAGATTTCTCCCGGAGCTACACGGGCTCTTACTCCGGGGA	694		
495	CCATCTCTGGGGGCT	CGGGGCAAGAAATTTCTCCCGAAGCTACACGGGCTGCTTACTCCCGAGA	554		
695	TGCTGCGCCGTGAT	TGGCCTGGAGAGCCCGCTGGGGTCAAGAGTGATCTCAGCAATGA	754		
555	TGGCGGAGATGAGT	AGTGGAGCTGGAAAGACAGATGGGGGTCAAGAGGTGATTCGGGTAAAGA	614		
755	GGACCTGAGGAGT	AGTGCAGAGACCTTGGGGCCCCCAATGGTTGGCCGACCTGGTTCG	814		
615	GGATCTGGGGGAGT	GTGGCTGGAAGATCTGGGGCCCCCAATGGTGGGCCCGTGGTCCG	674		
815	CTTCTACCCCGGGCT	GTGACCGGGTATGATGTCTGTCTGGGGGTGAGAGCTATAGGCTG	874		
675	TTTCTACCCCAAGG	CTGACCGGGTATGATGTCTGTCTGGGGGTGAGAGCTATAGGCTG	734		
875	CTCTGTGAGGAGT	CTGTCTTACACCGCCCTTGGGGCGAGACATGTATTTATC	934		
735	CTCTGTGAGGAGT	CTGTCTTACACCGCCCTTGGGGCGAGACATGTATTTATC	794		
935	TGAGAGCCTGTACT	CAACAGACTCCACTATGACGGACATACCGTGGGGCGAGCTGACATA	994		
795	TGAGATGGTGTAT	CTCATGATTCACACTTACAGATGGATGATCTGTGTGAGGGGCTGCACTA	854		

